

REMARKS

These remarks are in response to the Office Action mailed October 21, 2004. The specification has been amended to identify parts A-E and A-G in figures 2 and 24, respectively. Applicants have canceled claim 36, without prejudice to Applicants' right to prosecute the canceled subject matter in any divisional, continuation, continuation-in-part, or other application. Claims 5-31 and 33-35 have been canceled as directed to a non-elected invention. Figures 14 and 27 have been amended to correct a sequence error as clearly evident by the publicly available sequences and to correct typographical errors. No new matter is believed to have been introduced.

Applicants acknowledge the Examiner's indication that claims 1-2, 32 and 37 are allowable.

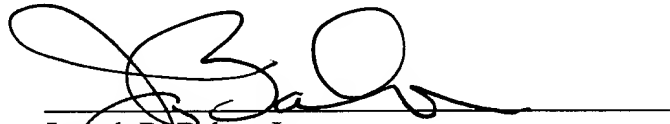
The rejections over claim 36 are now moot.

Please apply any other charges or credits to deposit account 06-1050.

Respectfully submitted,

Date: _____

10/28/04



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IN THE DRAWINGS:

Attached hereto are replacement sheets of drawings. Please substitute each of the drawings for the drawings currently on file.

The attached replacement sheets of drawings include changes to Figs. 14 and 27. Attached hereto are marked up copies of Figs. 14 and 27 showing the changes made in red ink. A clean copy of the figures are also included with the substitute figures.

The amendments to Fig. 14 correct the sequence number as evidence by counting of the respective amino acids. FIG. 27 corrects a typographical error in the sequence. The proper amino acid is recited in the sequence listing (See, SEQ ID NO:59) and as clearly evident by the published sequences available to one of skill in the art.



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Motif I			
RecJ_Tt	[73]	KRIRVHGDDADGLTGTAIVRGLAALG	[100]
RecJ_Ec	[73]	TRIIIVVGDFDADGATSTALSVLAMRSLG	[100]
RecJ_Aa	[78]	KRIIIYGDYDVGITGTAILYRVLKLLG	[105]
RecJ_Hp	[47]	TEILVVGDDADGVISSAIMAKFFESLN	[74]
RecJ_Hi	[68]	QKIVIVGDFDADGATSTALSVALRQLG	[95]
PPX1_Sc	[30]	TICVGNESADMSIASAITTSYCOYIYN	[57]
PRUNE_Dm	[37] 38	HLVMGNESCOLDSAVSAVTLAFVYAASS	[60] 65
		Motif II	Motif III
RecJ_Tt	[129]	SDLFLITVDCGITNHAELRE	[147] [153] VEVIVTPHHTPGK [165]
RecJ_Ec	[131]	AQLIVITVDNGISSHAGVEH	[149] 149 [155] IPVIVTPHHLPD [165] 167
RecJ_Aa	[133]	GDFLIITVDNGTSAVEEIDQ	[151] [154] LETVVIIPHNVPP [166]
RecJ_Hp	[102]	APLIITVDNGINAFEAAARF	[120] [126] YTLIITPHHCLHH [138]
RecJ_Hi	[126]	VQLLMTVDNGVSSFDGVAF	[144] [150] IRVLVTPHHLPPE [162]
PPX1_Sc	[120]	ELNSYLVDDNNDTPKNLKNY	[138] [141] NVVGIIDHFDLQ [153]
PRUNE_Dm	[88]	PLVCEMWDRCRARVALPRRY	[106] [129] NVTEILDHRPLED [141]
		Motif IV	Specific Motif
RecJ_Tt	[210]	YADLAAGVTIADVAPLWG	[228] [386] DLLLRYGGHKEAAGFAM [402]
RecJ_Ec	[226]	LLDLVALGTADVVPDLAN	[244] [422] GMMLKFGGHAMAAGLSL [438]
RecJ_Aa	[215]	FLDLVALGLADYMPVNPV	[233] [404] DMFLKWGGHOKAMGLTL [420]
RecJ_Hp	[189]	LLCLAGVATIADMMPLTFF	[207] [372] SLLGYGGHRQACGLSV [388]
RecJ_Hi	[219]	LLDLVALGTADVVPDLQN	[237] [415] NMILKFGGHAMAAGLSI [431]
PPX1_Sc	[191]	IALLLMGATLIDTSNMRK	[209]
PRUNE_Dm	[183]	VAQLLHATIVLDITNFAPA	[201]

Tt : Thermus thermophilus HB8, Ec : Escherichia coli, Aa : Aquifex aeolicus,
 Hp : Helicobacter pylori, Hi : Haemophilus influenzae Rd,
 Sc : Saccharomyces cerevisiae, Dm : Drosophila melanogaster

FIG. 14



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	10	20	30	40	50	60
Tth	MRLLFRQNFNRNLALEYRPPPGLSALVGANAQGKTSLLLGTHDA--LGGEVPLGL					
Eco	MSLTRLTRDFERNIETADALSPPGENFLVGANGSGKTSVLEAIYTLGHGRAFRSLQII					
Ppu	MSLRLRLMTAVRNLIHPVTLLPSPRINILYVGANGSGKTSVLEAVHLLGLARSLFRSTRLL					
Bsu	MYTIQNLCLTSYRNIDHAELQFENXVNVITIGENAQGKTNLMEAIYVL SMAKSHRTSND					
Mtu	MYVRLHGLRDFRSWACVDLELHPGRITVIVGPNQYGKTNLIEALWYSTTLGSHRVSAD					
Dra	MGDVRLSALSTLNVRNLA PGTLNFP EGVITGTYGENGAGKTNLLEAAYLA-LTGQTDAPRI					
	M L L - -RN- L PG- - -G NG GKT LLEA- - - R- -					
	70	80	90	100	110	120
Tth	ADLVRFGEELAWLHAEVETELG--AYRLEHRLGPGGREVLNGKR-VSLRTLWEIPGSV					
Eco	GRVIRHEQEAFLHGRLOGEER-ETATGLTKDKQ-GDSKVRIDGTDGKVAELAHLMPMQ					
Ppu	NPVIOYQAACTVFGVOLTEGGTSNLGVSRERQ-GEFTLRID-----ALKPVF					
Bsu	KELIRWQDYAKIEGRVMKQNG--AIPMOLVISKKGKKGKVNHIQQKLSQYVGALNTI					
Mtu	LPLIRVGTDRAVISTIVVNDGR-ECAYDL EATG-RVNKAARLNRSVSTRDVGVLRAV					
Dra	EQLIQAGETEAYVRADLOQGGG--LSIQEIVGLGRGRRLKVDGVRARTGDLR--RGGAV					
	LIR - - A - V- A- - - G - - - -					
	130	140	150	160	170	180
Tth	LVSPLDLEAVLGPKEERRIAYLDRLLIAHFSRRYAALLSAYEKAIRORNALLKAGG----					
Eco	LITPEGFTLLNGGPKYRRALFDWGCFFHNEPGFFTAWSNLKRLLKORNAARQVT--RY--					
Ppu	ERTLSELVELDGL-----					
Bsu	MFAPEDLNLVKGSPIQVRRRIFLDMEIGQVSPVYLHDLISLYOKILSORNHFLKLOLTRKQTD					
Mtu	LFAPEDLGLVRGDPADRRRIYLDLDAIVRRPATAAVRAEYERVLQRRTALLKSVPGARYRG					
Dra	WIRPEDSELVFGPPSGRRRIAYLDSLLSRLSARYGEQLSRYERTVSORNAALRGEE-----					
	- -PEDL LV G P RR -LD - - - S Y-- L QRNAL-					
	190	200	210	220	230	240
Tth	-----EGLSAWDRELARYGDEIVALLRRRFLRRIFAP-----ILREVHAALAAKEAGLR					
Eco	-----EQLRPWDKELIPLAEQISTWRAEYSAGTAADMADTCKQFLPEF-SLTESFORGWE					
Ppu	-----LTLSSYVRGWD					
Bsu	R-----TMDVLTDOVEVAAKVIVVKRLQFTAQLEKWAQPIHAGISRGLEELTLKYHTALD					
Mtu	DRGVFDTLDLWDSRLAEHGAELVAARIDLVNQLAPEVKKAYQLAPESRSASIGYRASMD					
Dra	-----WAMHVWDVLLKLGTEIMLRRRLTRLD-----ELAREANAQLGSRTLA					
	L WD L - - - R - - -					
	250	260	270	280	290	300
Tth	EETAGEG-VLRAIEASRAE-----ERE--RGOTLVGPHRDDLVLEGRPAHRIASR					
Eco	KE--TE---YAEVLERNFE-----RDRO--LTYYAHGPHKADLRIRADGAPVEDTLNR					
Ppu	KD--RE---LOEVLAISLL-----RDQO--MGHTQAGPORADLRRLTAGNNADILSR					
Bsu	VSDPLDLISKIGDSYQEAFSK-----LREKEIERGVITLSGPHRDDVLIFYVNGRDVQTYGSQ					
Mtu	VTGPSEQSDIDROTLAARLLAALAARDAELERGVCLVGPHRDDLIIRLGDQPAKGFAISH					
Dra	LTLTES---TSPETYAADLRG---RRAEELARGSTVITGPHRDDLLLTIGDFPASDYASR					
	- - - A- R--E RG T- GPHRDDL-- LG PA - SR					
	310	320	330	340	350	360
Tth	GEAKTLALALRLAEHRLGHHGEPILLVDEWGEELDEARRRIVLAYAQALPOATLAGL					
Eco	GOLKLLMCAALRLAQGEFLTRESGRRCLYLIDDFASELDDERRGLIASRLKATQSQVVFVSA					
Ppu	GOQKLLVVCALRLTAQGHVISOARRGHCILYLVDDLPSELDDOHRRLALCRLLEELRCOCSSPY					
Bsu	GOQRTTALSLLKLAIEDLIHEEIGEYPIILLDDVLSELDDYRQSHLLHTTIQG-RVOTFVTI					
Mtu	GEAWSLAVIALRLAAYQLTRVD--GGEPVILLDDVFAELDVMRRRIALATAAES-AEQVLVTA					
Dra	GEGRTVALIALRLAELLELREKFGEDPVLLLDLDDFTAEIDPHRRQYLLDLAASVPAQIVTGT					
	G- - - -A-ALRLA- LL - G P-LL-DD -ELD- RR- L - - Q- -					
	370	380	390			
Tth	EAPPGVVPCSVVRIGVVLCPGA			343		
Eco	ISAHVIDMSDENSKMFTVEKGKITD			357		
Ppu				233		
Bsu	TSVDGTTDHETLRQAGMFRVQNGALVK			370		
Mtu	AVLEDLPAGWDARRVHIDVRADDTGSM SVLP			385		
Dra	ELAPGAALTLRQAAGRFTPVADEEMQAEGTA			359		

Tth: Thermus thermophilus HB8
Eco: Escherichia coli
Ppu: Pseudomonas putida
Bsu: Bacillus subtilis
Mtu: Mycobacterium tuberculosis
Dra: Deinococcus radiodurans

FIG. 27